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1/19

FIGURE 1-1

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2/19

FIGURE 1-2

220	240	260	
272 K A N V T N L L I A N L A F S D F L M C			331 91
280	300	320	
332 C T C C T G C C A G C C G C T G A C C G C T A C A C C A T C A T G G A C T A C T G G A T C T T G G A G G			391 111
92 L L C Q P L T A V Y T I M D Y W I F G E			
340	360	380	
392 A C C C T C T G C A A G A T G T C G G C C T T C A T C C A G T G C A C G G T C T C C A T C C C T C T C G			451 131
112 T L C K M S A F I Q C H S V T V S I L S			
400	420	440	
452 C T C G T C C T C G T G G C C T G G A G G C A T C A G G C T C A T C A T C A A C C C A A C A G G C T G G A A G C C C			511 151
132 L V L V A L E R H Q L I I N P T G W K P			
460	480	500	
512 A G C A T C T C A C A G G C C T A C C T G G G A T T T G T G C T C A T C T G G G T C A T T G C C T C T G T C C T C C			571 171
152 S I S Q A Y L G I V L I W V I A C V L S			

3/19

FIGURE 1-3

520	CTGCCCTTCCTGGCCAAACAGCATCCTGGAGAATGTCCTTCCACAAGAACCAACTCCAAGGCT	560
172	L P F L A N S I L E N V F H K N H S K A	191
580	CTGGAGTTCCCTGGCGAGATAAGGTGGCTCTGACCGAGTGCCCTGGCCACTGGCTCACACC	620
192	L E F L A D K V V C T E S W P L A H H R	211
640	660	680
212	T I Y T T F L L F Q Y C L P L G F I L	231
700	720	740
232	V C Y A R I Y R R L Q R Q G R V F H K G	251
760	780	800
252	T Y S L R A G H M K Q V N V L V M V	271

4/19

FIGURE 1-4

872	G	T	G	G	C	T	T	G	C	T	T	G	A	A	G	A	C	T	G	A	C	931		
272	V	A	F	A	V	L	W	L	P	L	H	V	F	N	S	L	E	D	W	H	291			
880																								
840																								
932	C	A	T	G	A	G	G	C	A	C	G	G	A	A	C	T	C	T	G	C	T	T	G	991
292	H	E	A	I	P	I	C	H	N	L	I	F	L	V	C	H	L	L	A	311				
940																								
860																								
992	A	T	G	G	C	T	C	A	A	C	C	C	A	T	C	A	A	C	A	T	C	A	G	1051
312	M	A	S	T	C	V	N	P	F	I	Y	G	F	L	N	T	N	F	K	K	331			
1000																								
820																								
1052	G	A	G	T	C	A	G	G	C	A	G	G	G	G	C	C	C	C	T	G	A	G	T	1111
332	E	I	K	A	L	V	L	T	C	Q	Q	S	A	P	L	E	E	S	E	H	351			
1060																								
1080																								
1112	C	T	G	C	C	A	C	A	G	T	A	C	G	A	G	T	C	C	C	T	G	A	G	1171
352	L	P	L	S	T	V	H	T	E	V	S	K	G	S	L	R	L	S	G	R	371			

5/19

FIGURE 1-5

1172	TCCAATCCATTAAACCAAGGTCTAGGTCTTCTCCCATGCCATTGTCCTGGCCTCTTC	1140	1160	1231
372	S N P I *			375
1180		1200	1220	
1232	CACTTAGCTTAAGTGGCACACTGCAAGCTGGGTGGCACCCCCAGGCATTCCCTGGCTTC			1291

6/19

FIGURE 2-1

FIGURE 2-1
FIGURE 2-2
FIGURE 2-3

<p>hp25a human Y1 rat Y1 mouse Y1</p> <p>1</p>	<p>51 I hp25a human Y1 rat Y1 mouse Y1</p>	<p>50</p>	<p>51 II hp25a human Y1 rat Y1 mouse Y1</p>	<p>100</p>	<p>101 III hp25a human Y1 rat Y1 mouse Y1</p>	<p>150</p>	<p>151 IV hp25a human Y1 rat Y1 mouse Y1</p>	<p>200</p>
<pre> MNTSHILLALL LPKSPQGENR SKPLGTPYNP SEHCQDSVDY MVFIVTSSSI MN. STIFSOV ENHSTHSNFS ETKAQLLAFAE NDDCHLPLAM IFTLALAYGA MN. STIFSRV ENY SVHYNVS E. NSPFLAFAE NDDCHLPLAV IFTLALAYGA MN. STIFSKV ENHSTIHYNAS E. NSPLLAFAE NDDCHLPLAV IFTLALAYGA </pre>								

7/19

FIGURE 2-2

	hp25a	human Y1	rat Y1	mouse Y1	201	250	300	350
						V		
	CTESWPLAHH	RIVTTPEHL	FQVCLPICKI	LVCYARIYPR		LRQGRVFHK		
	CFDGFPSDSH	RLSITVLLV	LOVFGPLCPTI	FICYFKIVIR		LKRRNNMMDK		
	CFDKFPPSDSH	RLSITVLLV	LOVFGPLCPTI	FICYFKIVIR		LKRRNNMMDK		
	CFDKFPPSDSH	RLSITVLLV	LOVFGPLCPTI	FICYFKIVIR		LKRRNNMMDK		
						VI		
	GTYSLRACH	MKQVNYYVV	MVVAFAVLLI	PLHVPLNSLED		VNHQIATCN		
	MRDNKYRSSE	TKRINIMLIS	IIVAAFAVCII	PITIFNTVFD		VNHQIATCN		
	IRD\$KYRSSE	TKRINIMLIS	IIVAAFAVCII	PITIFNTVFD		VNHQIATCN		
	IRD\$KYRSSE	TKRINIMLIS	IIVAAFAVCII	PITIFNTVFD		VNHQIATCN		
						VII		
	GMIIFLYCHI	LAMASTCVNP	FIVGELNKNE	KKEIKALVLT		QQQSAPLEES		
	HNLFLYLCHI	TAMISTCVNP	IFVGELNKNE	ORDIQFFFNF		CDFRSRDDY		
	HNLFLYLCHI	TAMISTCVNP	IFVGELNKNE	ORDLQFFFNF		CDFRSRDDY		
	HNLFLYLCHI	TAMISTCVNP	IFVGELNKNE	ORDLQFFFNF		CDFRSRDDY		

8/19

FIGURE 2-3

351	PHPLSTVHT	EVSYKCAIRLS	GRSNPI*...*...*...*
	ETIAMSTMH	DYSKTKQAA	SPVAFKKINN NDDNEKI*
	ETIAMSTMH	DYSKTKQAA	SPVAFKKISM N.DNEKI*
	ETIAMSTMH	DYSKTKQAA	SPVAFKKISM N.DNEKV*
hp25a			
human Y1			
rat Y1			
mouse Y1			

9/19

FIGURE 3-1

FIGURE 3-1
FIGURE 3-2
FIGURE 3-3
FIGURE 3-4

-170

-150

-130

ATAGCTCTCAAGCCATAAGATATAAGTAGCTAAGAATTGTCTCCCTCTCCGTCCCTTG

-110

-90

-70

TTCTTACCTGGTTCATTTACATGCCTGGACCTTGAGTTCCATTGTTGTTGCAG

-50

-30

-10

GCTACACTCAGAAGTGGGCCCTTAGTCTTGAAGTTCTGGCTTCTCACACCCACCATG

M

10

30

50

AATACCTCTCATCTCATGGCCTCCCTTCTCCGGCATTCTACAAGGTAAGAATGGGACC
N T S H L M A S L S P A F L Q G K N G T

70

90

110

AACCCACTGGATTCCCTCTATAATCTCTGACGGCTGCCAGGATTGGCAGATCTGTTG
N P L D S L Y N L S D G C Q D S A D L L

130

150

170

GCCTTCATCATCACCAACCTACAGCGTTGAGACCGCTTGGGGTCTAGGAAACCTCTGC
A F I I T T Y S V E T V L G V L G N L C

190

210

230

TTGATATTTGTGACCACAAGGAAAAGGAAATGCTTCAATGTGACCAACCTACTCATTGCC
L I F V T T R Q K E K S N V T N L L I A

10/19

FIGURE 3-2

250 270 290
AACCTGGCCTCTCTGACTTCCTCATGTGTCTCATGCCAGCCGCTCACGGTACCTAC
N L A F S D F L M C L I C Q P L T V T Y

310 330 350
ACCATCATGGACTACTGGATCTCGCGAAGTCCTTGCAAGATGTTAACGTTCATCCAG
T I M D Y W I F G E V L C K M L T F I Q

370 390 410
TGTATGTCGGTGACAGTCTCCATCCTCTCACTGGCCTTGTGGCCCTGGAGAGGCACCAAG
C M S V T V S I L S L V L V A L E R H Q

430 450 470
CTCATTATCAACCCGACTGGCTGGAAACCCAGCATTCCCAGGCCTACCTGGGGATTGTG
L I I N P T G W K P S I S Q A Y L G I V

490 510 530
GTCATCTGGTTCAATTCTTGTTCCTCTCCTGCCCTGCCATAGCATCCTGAAC
V I W F I S C F L S L P F L A N S I L N

550 570 590
GACCTCTTCCACTACAACCACTCTAAGGTTGTGGAGTTCTGGAAGACAAGGTTGTCTGC
D L F H Y N H S K V V E F L E D K V V C

610 630 650
TTTGTGTCTGGTCCTCGGATCACCAACCGCCTCATCTACACCAACCTTCTGCTGCTCTC
F V S W S S D H H R L I Y T T F L L L F

11/19

FIGURE 3-3

670 690 710

CAATACTGCGTCCCTCTGGCCTCATCCTGGTCTGCTACATGCGTATCTATCAGCGCCTG
 Q Y C V P L A F I L V C Y M R I Y Q R L

730 750 770

CAGAGGCAGAGGCGTGCCTCACACGACACTTGAGCTCACGAGTGGGCAGATGAAG
 Q R Q R R A F H T H T C S S R V G Q M K

790 810 830

CGGATCAATGGCATGCTCATGGCAATGGTACTGCCCTTGAGTTCTGGCTGCCCTG
 R I N G M L M A M V T A F A V L W L P L

850 870 890

CATGTGTTAACACTGGAGGACTGGTACCAAGGAAGCCATCCCTGCTTGCATGGCAAC
 H V F N T L E D W Y Q E A I P A C H G N

910 930 950

CTCATCTTCTTGATGTGCCACCTGTTGCCATGGCTTCCACCTGTGTCACCCCTTCATC
 L I F L M C H L F A M A S T C V N P F I

970 990 1010

TATGGCTTCTAACATCAACTCAAGAAGGACATCAAGGCTCTGGTTCTGACCTGCCGT
 Y G F L N I N F K K D I K A L V L T C R

1030 1050 1070

TGCAGGCCACCTCAAGGGAGCCTGAGCCTCTGCCCTGTCCACTGTGCACACGGACCTC
 C R P P Q G E P E P L P L S T V H T D L

12/19

FIGURE 3-4

1090

1110

1130

TCCAAGGGATCTATGAGGA~~T~~GGTAGCAAGTCTAACGT~~C~~TGAGTCATGTCTAGGCTCT
S K G S M R M G S K S N V M *

1150

1170

1190

TCCGCCATTTC~~T~~TCGACACACC~~T~~TTCACTGAGCTAAGTAGACACAATGCAAGCTGTG

1210

1230

1250

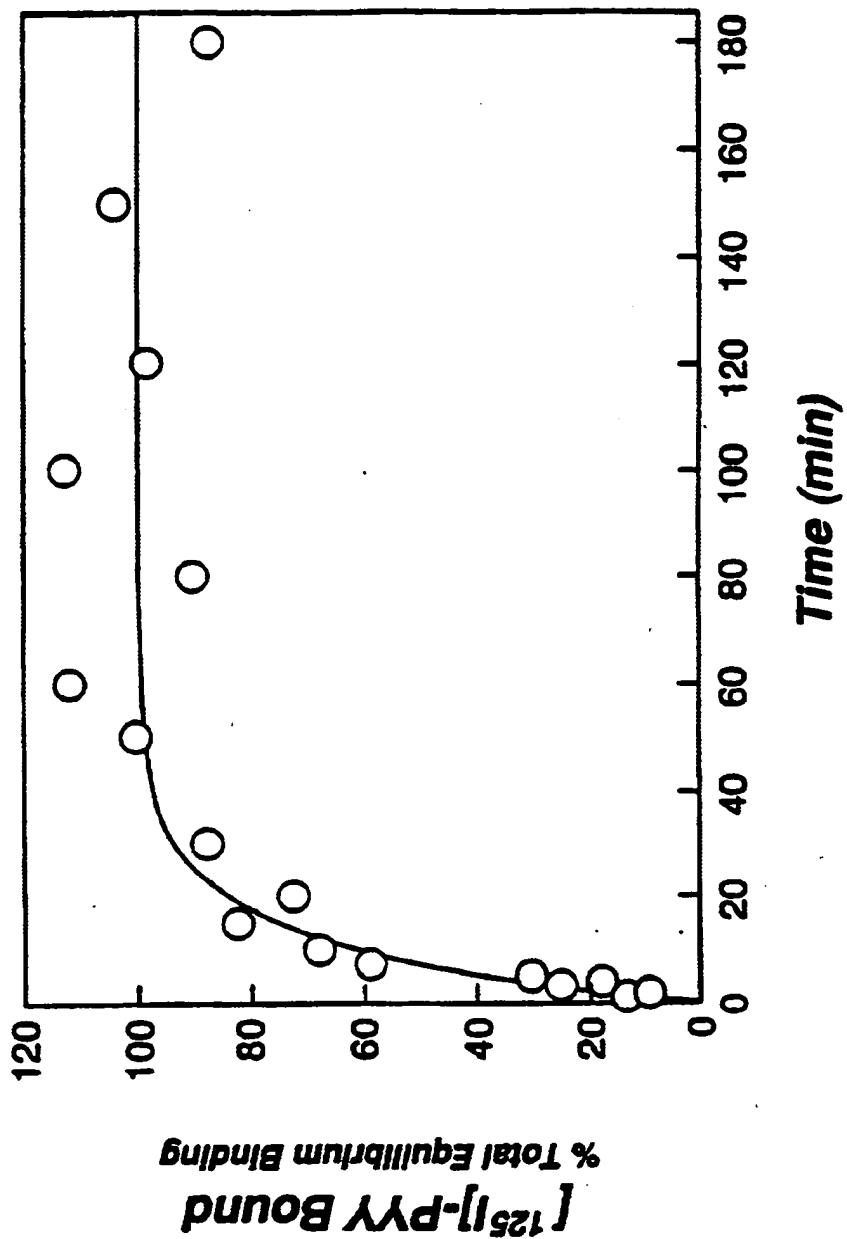
GTATCATCCTGCCATTCTGGT~~T~~GGGCCAGACAGGCGGCAAGAGACTTGAAGCTT

13/19

FIGURE 4

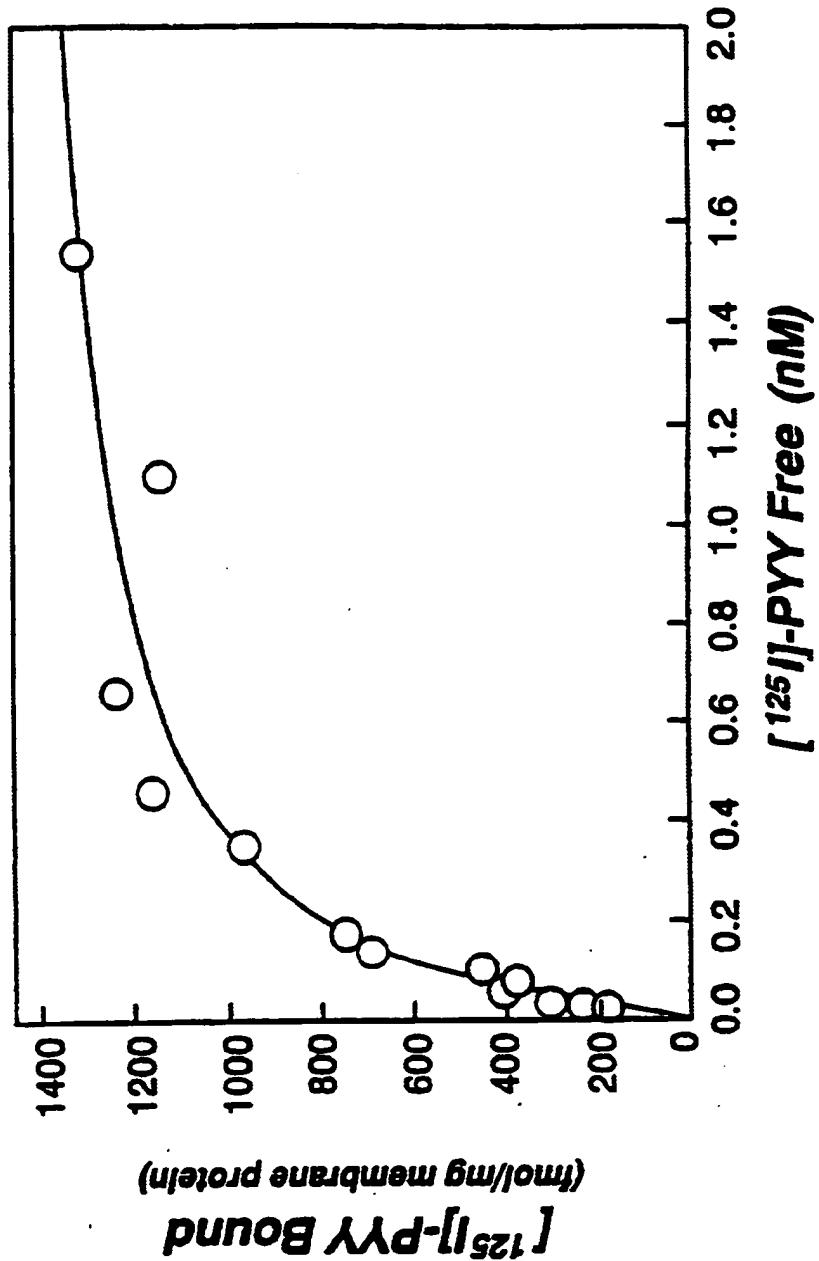
1	50
<hr/>	
Y4rat MNTSHLMASL SPAFLQGKNG TNPLDSLYNL SDGCQDSADL LAFIITTYSV	
Y4hum MNTSHLLALL LPKSPQGENR SKPLGTPYNF SEHCQDSVDV MVFIVTSYSI	
<hr/>	
51	100
<hr/> I <hr/>	
Y4rat ETVLGVLGNL CLIPVTTRQK EKSNVTNLLI ANLAFLSDFLM CLICQPLTVT	
Y4hum ETVVGVLGNL CLMCVTVRQK EKANVTNLLI ANLAFLSDFLM CLLCQPLTAV	
<hr/>	
101	150
<hr/> II <hr/>	
Y4rat YTIMDYWIPG EVLCRMLTFI QCMSVTVSIL SLVLVALERH QLIINPTGWK	
Y4hum YTIMDYWIPG ETLCRMSAFI QCMSVTVSIL SLVLVALERH QLIINPTGWK	
<hr/>	
151	200
<hr/> III <hr/>	
Y4rat PSISQAYLGI VVINFISCPL SLPFLANSIL NDLFHYNHSK VVEFLEDKV	
Y4hum PSISQAYLGI VLIWVIACVL SLPFLANSIL ENVFKHNHSK ALEFLADKV	
<hr/>	
201	250
<hr/> IV <hr/>	
Y4rat PSISQAYLGI VVINFISCPL SLPFLANSIL NDLFHYNHSK VVEFLEDKV	
Y4hum PSISQAYLGI VLIWVIACVL SLPFLANSIL ENVFKHNHSK ALEFLADKV	
<hr/>	
251	300
<hr/> V <hr/>	
Y4rat CFVSWSSDH H RLIYTTPLL PQYCVPLAFI LVCYMR I YQR LQRQRRAFH T	
Y4hum CTESWPLAH H RTIYTTPLL PQYCLPLGFI LVCYARIYRR LQRQGRVPH K	
<hr/>	
301	350
<hr/> VI <hr/>	
Y4rat HTCSSRVGQM KRINGMLMAN VTAPAVLWLP LHVPNTLEDW YQRAIPACHG	
Y4hum GTYSRLRAGHM KQVNVLVVM VVAPAVLWLP LHVPNSLEDW HHEAIPICHG	
<hr/>	
351	400
<hr/> VII <hr/>	
Y4rat NLIFLMCHLF AMASTCVNPF IYGFLNINFK KDIKALVLTC RCRPPQGEPE	
Y4hum NLIFLVCHLL AMASTCVNPF IYGFLNINFK KEIKALVLTC QQSAPLEESE	

14/19

FIGURE 5

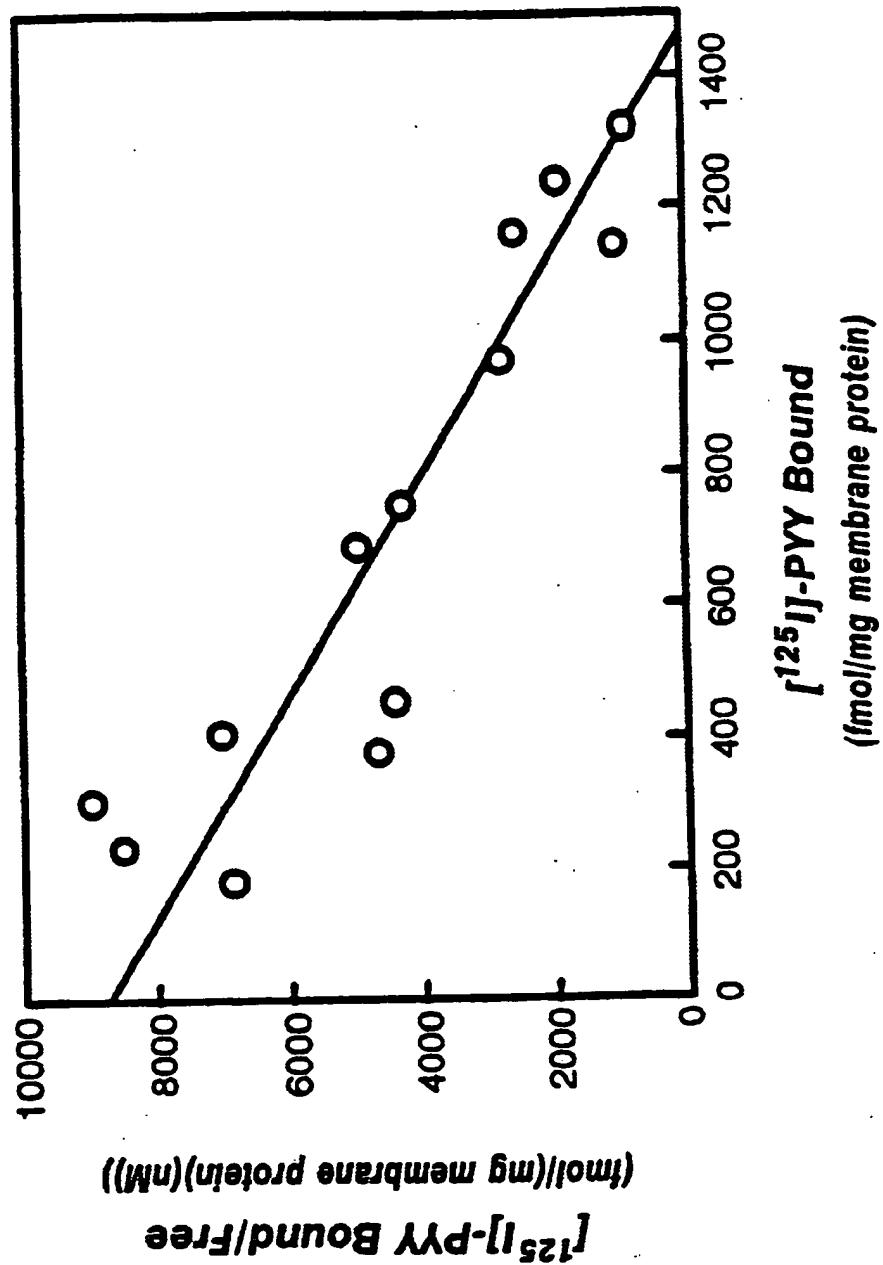
15/19

FIGURE 6A



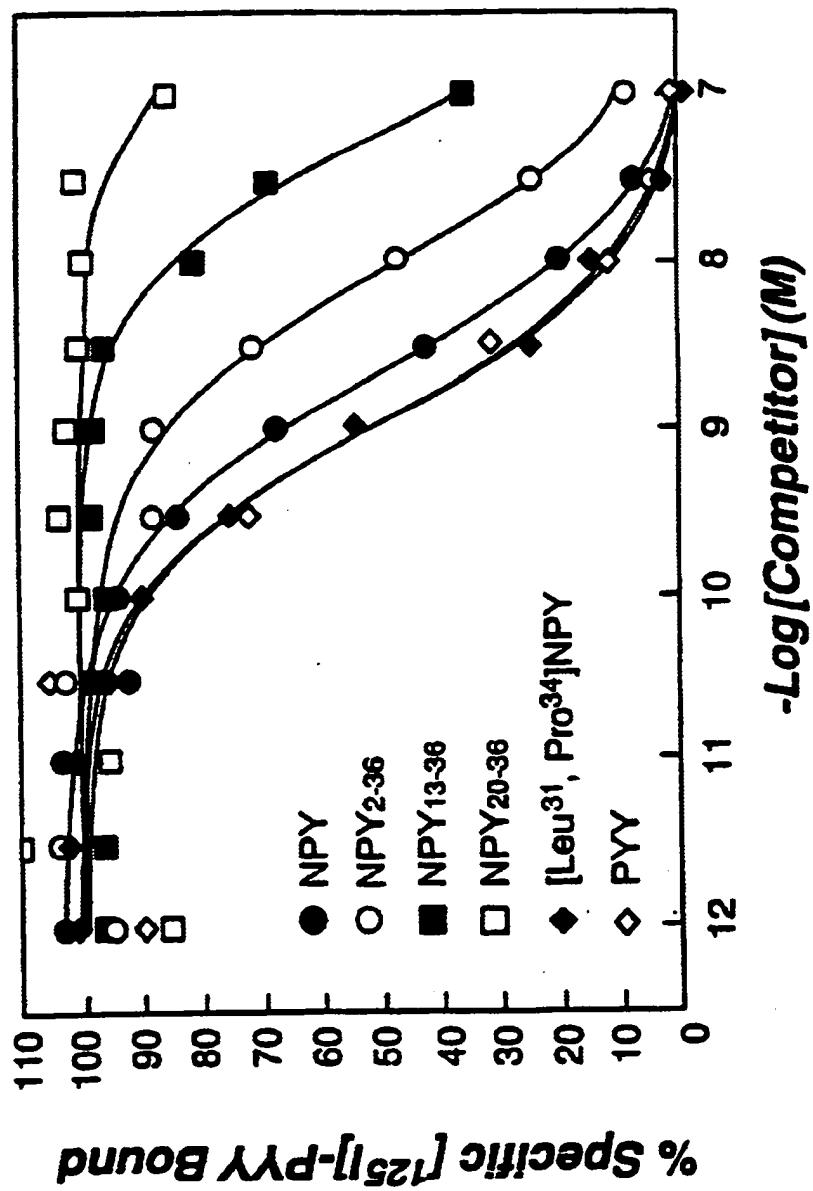
16/19

FIGURE 6B

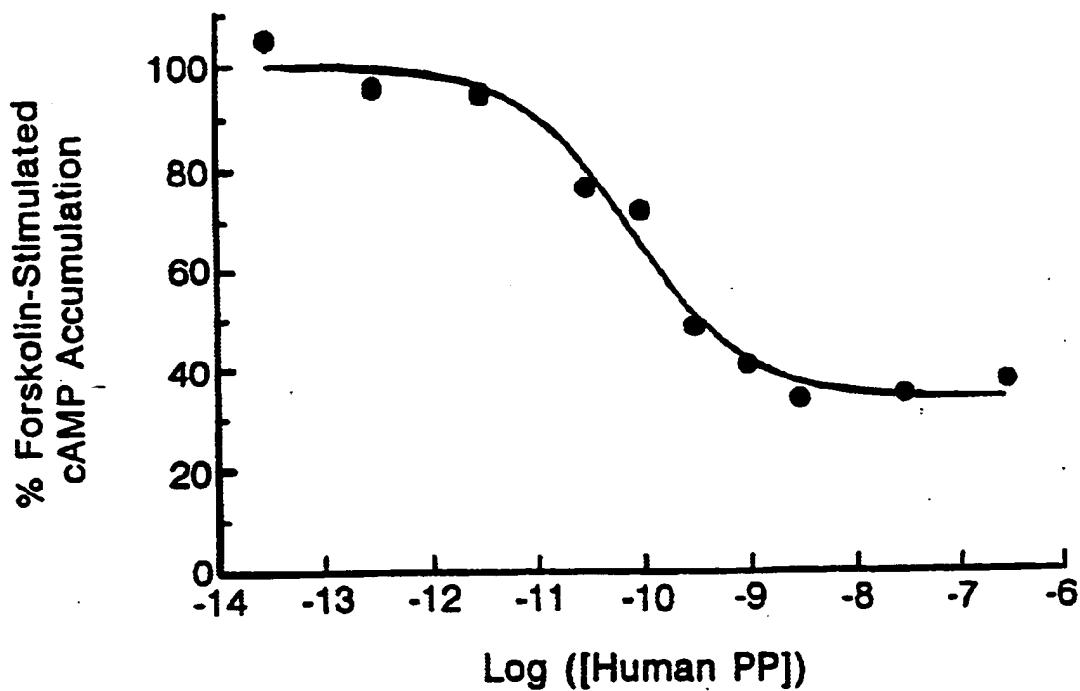


17/19

FIGURE 7



18/19

FIGURE 8

19/19

FIGURE 9A

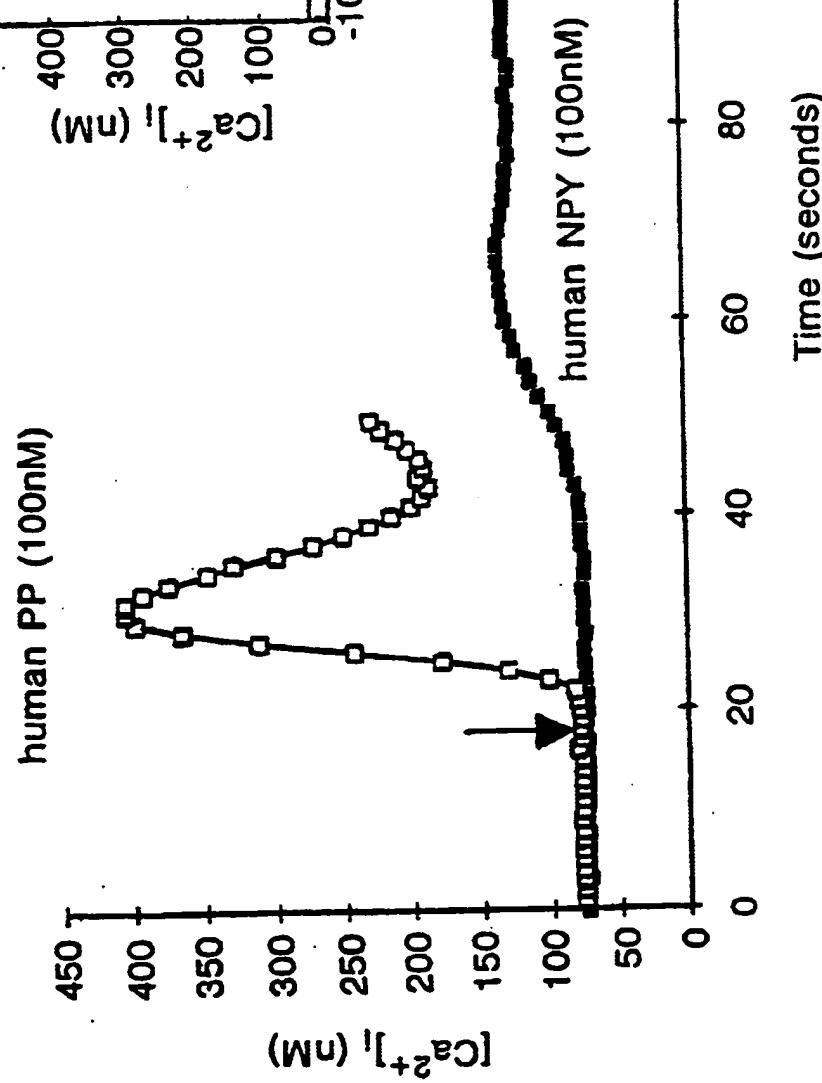
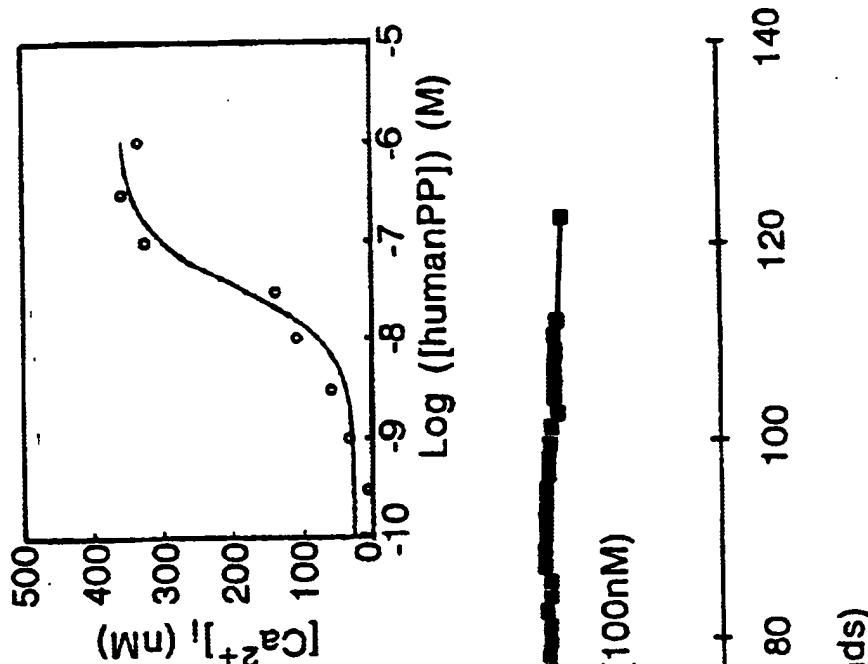


FIGURE 9B



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